



SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger

<120> Novel chimeric plasminogen activators and their pharmaceutical use

<130> 607927-000001

<140> US/10/583,785

<141> 2006-06-19

<160> 26

<210> 1

<211> 1143

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1143)

<223> Coding sequence of the surfactant protein B precursor

<400> 1

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	

130	135	140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg			480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu			
145	150	155	160
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc			528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu			
	165	170	175
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac			576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His			
	180	185	190
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc			624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys			
	195	200	205
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag			672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys			
	210	215	220
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg			720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu			
	225	230	235
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc			768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile			
	245	250	255
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc			816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg			
	260	265	270
ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tgc ccg			864
Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro			
	275	280	285
aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc			912
Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser			
	290	295	300
gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca			960
Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala			
	305	310	315
atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag			1008
Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys			
	325	330	335
caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg			1056
Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg			
	340	345	350
ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc			1104
Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr			
	355	360	365

atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt	1143
Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu	
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<210> 2

<211> 837

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

<400> 2

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	

ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	

gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	

aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	

ggc ggc cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	

gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	

ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	

ctc gtc ctc cgg tgc tcc atg	837
Leu Val Leu Arg Cys Ser Met	
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<210> 3
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (237)
 <223> Coding sequence of the mature surfactant protein B

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cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc	96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala	
20 25 30	

cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc	144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys	
35 40 45	

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc	192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg	
50 55 60	

atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg	237
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<210> 4
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (1293)
 <223> Coding sequence of the single-chain urokinase-plasminogen activator

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atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc	48
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1 5 10 15	

gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac	96
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp	
20 25 30	

tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att	144
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile	
35 40 45	

cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata	192
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile	
50 55 60	

gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga	240
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly	
65 70 75 80	

aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct	288
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser	
85 90 95	

gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt	336
Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu	
100 105 110	

cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg	384
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg	
115 120 125	

agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa	432
Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln	
130 135 140	

gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct	480
Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro	
145 150 155 160	
cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc	528
Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg	
165 170 175	
ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg	576
Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp	
180 185 190	
ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg	624
Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val	
195 200 205	
tgt gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac	672
Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His	
210 215 220	
tgc ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt	720
Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly	
225 230 235 240	
cgc tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg	768
Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val	
245 250 255	
gaa aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac	816
Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His	
260 265 270	
cac aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt	864
His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys	
275 280 285	
gcg cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat	912
Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr	
290 295 300	
aac gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa	960
Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys	
305 310 315 320	
gag aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt	1008
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val	
325 330 335	
gtg aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc	1056
Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly	
340 345 350	
tct gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa	1104
Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys	
355 360 365	

aca gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc	1152
Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu	
370 375 380	
caa ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt	1200
Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys	
385 390 395 400	
gcc ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta	1248
Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu	
405 410 415	
ccc tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc	1293
Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu	
420 425 430	
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<211> 828	
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<213> Homo sapiens	
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<221> CDS	
<222> (1) ... (828)	
<223> Coding sequence of low mw two-chain urokinase-plasminogen activator	
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Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys	
1 5 10 15	
act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc	96
Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile	
20 25 30	
gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc	144
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly	
35 40 45	
tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg	192
Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val	
50 55 60	
atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac	240
Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr	
65 70 75 80	
atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag	288
Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu	
85 90 95	
atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct	336
Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala	
100 105 110	

gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser 115 120 125	384
aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys 130 135 140	432
ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile 145 150 155 160	480
act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln 165 170 175	528
ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln 180 185 190	576
ccc cac tac tac ggc tct gaa gtc acc acc aaa atg ctg tgt gct gct Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala 195 200 205	624
gac cca cag tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro 210 215 220	672
ctc gtc tgt tcc ctc caa ggc cgc atg act ttg act gga att gtg agc Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser 225 230 235 240	720
tgg ggc cgt gga tgt gcc ctg aag gac aag cca ggc gtc tac acg aga Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg 245 250 255	768
gtc tca cac ttc tta ccc tgg atc cgc agt cac acc aag gaa gag aat Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn 260 265 270	816
ggc ctg gcc ctc Gly Leu Ala Leu 275	828

<210> 6

<211> 1671

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

<220>

<221> CDS

<222> (844) ... (1671)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 6

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg	48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr	
1 5 10 15	
ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt	96
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys	
20 25 30	
gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag	144
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln	
35 40 45	
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga	192
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly	
50 55 60	
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac	240
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn	
65 70 75 80	
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg	288
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu	
85 90 95	
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc	336
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys	
100 105 110	
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag	384
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln	
115 120 125	
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa	432
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys	
130 135 140	
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg	480
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu	
145 150 155 160	
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc	528
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu	
165 170 175	
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac	576
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His	
180 185 190	
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc	624
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys	
195 200 205	

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag	672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys	
210 215 220	
ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg	720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu	
225 230 235 240	
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc	768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile	
245 250 255	
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg	
260 265 270	
ctc gtc ctc cgg tgc tcc atg aag ctt aag ccc tcc tct cct cca gaa	864
Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu	
275 280 285	
gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag	912
Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys	
290 295 300	
att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg	960
Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala	
305 310 315 320	
gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga	1008
Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly	
325 330 335	
ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc	1056
Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe	
340 345 350	
att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca	1104
Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser	
355 360 365	
agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac	1152
Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn	
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Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn	
385 390 395 400	
gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag	1248
Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln	
405 410 415	
cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat	1296
Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp	
420 425 430	
ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat	1344

Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn		
	435						440					445					
tct	acc	gac	tat	ctc	tat	ccg	gag	cag	ctg	aaa	atg	act	gtt	gtg	aag	1392	
Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys		
	450					455					460						
ctg	att	tcc	cac	cgg	gag	tgt	cag	cag	ccc	cac	tac	tac	ggc	tct	gaa	1440	
Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu		
465					470					475					480		
gtc	acc	acc	aaa	atg	ctg	tgt	gct	gct	gac	cca	cag	tgg	aaa	aca	gat	1488	
Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp		
			485						490					495			
tcc	tgc	cag	gga	gac	tca	ggg	gga	ccc	ctc	gtc	tgt	tcc	ctc	caa	ggc	1536	
Ser	Cys	Gln	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly		
		500						505					510				
cgc	atg	act	ttg	act	gga	att	gtg	agc	tgg	ggc	cgt	gga	tgt	gcc	ctg	1584	
Arg	Met	Thr	Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu		
	515						520					525					
aag	gac	aag	cca	ggc	gtc	tac	acg	aga	gtc	tca	cac	ttc	tta	ccc	tgg	1632	
Lys	Asp	Lys	Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp		
	530					535					540						
atc	cgc	agt	cac	acc	aag	gaa	gag	aat	ggc	ctg	gcc	ctc				1671	
Ile	Arg	Ser	His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu					
545					550					555							

<210> 7

<211> 1674

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of SP-B precursor lacking the C-terminal propeptide

<220>

<221> CDS

<222> (847) ... (1674)

<223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<400> 7

atg	gct	gag	tca	cac	ctg	ctg	cag	tgg	ctg	ctg	ctg	ctg	ctg	ccc	acg	48	
Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr		
1				5				10						15			
ctc	tgt	ggc	cca	ggc	act	gct	gcc	tgg	acc	acc	tca	tcc	ttg	gcc	tgt	96	
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Thr	Thr	Ser	Ser	Leu	Ala	Cys		
			20					25					30				

gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln 35 40 45	144
tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly 50 55 60	192
gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn 65 70 75 80	240
aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu 85 90 95	288
gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys 100 105 110	336
aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln 115 120 125	384
aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys 130 135 140	432
tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu 145 150 155 160	480
ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu 165 170 175	528
gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His 180 185 190	576
aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys 195 200 205	624
tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys 210 215 220	672
ggc gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu 225 230 235 240	720
gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile 245 250 255	768
ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc	816

Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	
			260					265					270			
ctc	gtc	ctc	cgg	tgc	tcc	atg	cag	ata	tct	aag	ccc	tcc	tct	cct	cca	864
Leu	Val	Leu	Arg	Cys	Ser	Met	Gln	Ile	Ser	Lys	Pro	Ser	Ser	Pro	Pro	
			275				280					285				
gaa	gaa	tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	912
Glu	Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	
	290					295					300					
aag	att	att	ggg	gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	960
Lys	Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	
305					310					315					320	
gcg	gcc	atc	tac	agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	1008
Ala	Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	
				325					330					335		
gga	ggc	agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	1056
Gly	Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	
			340					345					350			
ttc	att	gat	tac	cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggg	cgc	1104
Phe	Ile	Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	
		355					360					365				
tca	agg	ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	1152
Ser	Arg	Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	
	370					375					380					
aac	ctc	atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	1200
Asn	Leu	Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	
385					390					395					400	
aac	gac	att	gcc	ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	1248
Asn	Asp	Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	
				405				410						415		
cag	cca	tcc	cgg	act	ata	cag	acc	atc	tgc	ctg	ccc	tgc	atg	tat	aac	1296
Gln	Pro	Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	
				420				425					430			
gat	ccc	cag	ttt	ggc	aca	agc	tgt	gag	atc	act	ggc	ttt	gga	aaa	gag	1344
Asp	Pro	Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	
		435					440					445				
aat	tct	acc	gac	tat	ctc	tat	ccg	gag	cag	ctg	aaa	atg	act	gtt	gtg	1392
Asn	Ser	Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	
	450					455					460					
aag	ctg	att	tcc	cac	cgg	gag	tgt	cag	cag	ccc	cac	tac	tac	ggc	tct	1440
Lys	Leu	Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	
465					470					475					480	
gaa	gtc	acc	acc	aaa	atg	ctg	tgt	gct	gct	gac	cca	cag	tgg	aaa	aca	1488
Glu	Val	Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	

485	490	495	
gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa			1536
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln			
500	505	510	
ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc			1584
Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala			
515	520	525	
ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc			1632
Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro			
530	535	540	
tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc			1674
Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu			
545	550	555	
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<211> 591			
<212> DNA			
<213> Homo sapiens			
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<221> CDS			
<222> (1) ... (591)			
<223> Coding sequence of the surfactant protein C precursor			
 <400> 8			
atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac			48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr			
1	5	10	15
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac			96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His			
20	25	30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg			144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val			
35	40	45	
gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac			192
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His			
50	55	60	
acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa			240
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln			
65	70	75	80
cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc			288
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile			
85	90	95	
ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc			336
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala			

100	105	110	
tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca			384
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro			
115	120	125	
gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc			432
Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe			
130	135	140	
cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag			480
Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys			
145	150	155	160
ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg			528
Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly			
165	170	175	
gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg			576
Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val			
180	185	190	
ccg ctc tac tac atc			591
Pro Leu Tyr Tyr Ile			
195			

<210> 9
 <211> 174
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (1) ... (174)
 <223> Coding sequence of SP-C precursor lacking the C-terminal propeptide

 <400> 9

atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac	48
Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr	
1 5 10 15	
tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac	96
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His	
20 25 30	
ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg	144
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val	
35 40 45	
gtg att gtg gga gcc ctg ctc atg ggt ctc	174
Val Ile Val Gly Ala Leu Leu Met Gly Leu	
50 55	

<210> 10

<211> 105
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (105)
 <223> Coding sequence of the mature surfactant protein C

<400> 10

ttt ggc att ccc tgc tgc cca	gtg cac ctg aaa cgc ctt ctt atc gtg	48
Phe Gly Ile Pro Cys Cys Pro	Val His Leu Lys Arg Leu Leu Ile Val	
1 5	10 15	

gtg gtg gtg gtg gtc ctc atc	gtc gtg gtg att gtg gga gcc ctg ctc	96
Val Val Val Val Val Leu Ile	Val Val Val Ile Val Gly Ala Leu Leu	
20	25 30	

atg ggt ctc	105
Met Gly Leu	
35	

<210> 11
 <211> 1686
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (1686)
 <223> Coding sequence of the tissue-plasminogen activator

<400> 11

atg gat gca atg aag aga ggg	ctc tgc tgt gtg ctg ctg ctg tgt gga	48
Met Asp Ala Met Lys Arg Gly	Leu Cys Cys Val Leu Leu Leu Cys Gly	
1 5	10 15	

gca gtc ttc gtt tcg ccc agc	cag gaa atc cat gcc cga ttc aga aga	96
Ala Val Phe Val Ser Pro Ser	Gln Glu Ile His Ala Arg Phe Arg Arg	
20	25 30	

gga gcc aga tct tac caa gtg	atc tgc aga gat gaa aaa acg cag atg	144
Gly Ala Arg Ser Tyr Gln Val	Ile Cys Arg Asp Glu Lys Thr Gln Met	
35	40 45	

ata tac cag caa cat cag tca	tgg ctg cgc cct gtg ctc aga agc aac	192
Ile Tyr Gln Gln His Gln Ser	Trp Leu Arg Pro Val Leu Arg Ser Asn	
50	55 60	

cgg gtg gaa tat tgc tgg tgc	aac agt ggc agg gca cag tgc cac tca	240
Arg Val Glu Tyr Cys Trp Cys	Asn Ser Gly Arg Ala Gln Cys His Ser	
65	70 75 80	

gtg cct gtc aaa agt tgc agc	gag cca agg tgt ttc aac ggg ggc acc	288
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Val	Pro	Val	Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr		
				85					90					95			
tgc	cag	cag	gcc	ctg	tac	ttc	tca	gat	ttc	gtg	tgc	cag	tgc	ccc	gaa		336
Cys	Gln	Gln	Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu		
			100					105					110				
gga	ttt	gct	ggg	aag	tgc	tgt	gaa	ata	gat	acc	agg	gcc	acg	tgc	tac		384
Gly	Phe	Ala	Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr		
		115					120					125					
gag	gac	cag	ggc	atc	agc	tac	agg	ggc	acg	tgg	agc	aca	gcg	gag	agt		432
Glu	Asp	Gln	Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser		
	130					135					140						
ggc	gcc	gag	tgc	acc	aac	tgg	aac	agc	agc	gcg	ttg	gcc	cag	aag	ccc		480
Gly	Ala	Glu	Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro		
145					150					160					165		
tac	agc	ggg	cgg	agg	cca	gat	gcc	atc	agg	ctg	ggc	ctg	ggg	aac	cac		528
Tyr	Ser	Gly	Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His		
			170						175					180			
aac	tac	tgc	aga	aac	cca	gat	cga	gac	tca	aag	ccc	tgg	tgc	tac	gtc		576
Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val		
			185					190					195				
ttt	aag	gcg	ggg	aag	tac	agc	tca	gag	ttc	tgc	agc	acc	cct	gcc	tgc		624
Phe	Lys	Ala	Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys		
	200						205					205					
tct	gag	gga	aac	agt	gac	tgc	tac	ttt	ggg	aat	ggg	tca	gcc	tac	cgt		672
Ser	Glu	Gly	Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg		
	210					215					220						
ggc	acg	cac	agc	ctc	acc	gag	tgc	ggt	gcc	tcc	tgc	ctc	ccg	tgg	aat		720
Gly	Thr	His	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn		
225				230					235					240			
tcc	atg	atc	ctg	ata	ggc	aag	gtt	tac	aca	gca	cag	aac	ccc	agt	gcc		768
Ser	Met	Ile	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala		
			245					250						255			
cag	gca	ctg	ggc	ctg	ggc	aaa	cat	aat	tac	tgc	cgg	aat	cct	gat	ggg		816
Gln	Ala	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly		
			260				265						270				
gat	gcc	aag	ccc	tgg	tgc	cac	gtg	ctg	aag	aac	cgc	agg	ctg	acg	tgg		864
Asp	Ala	Lys	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp		
		275					280					285					
gag	tac	tgt	gat	gtg	ccc	tcc	tgc	tcc	acc	tgc	ggc	ctg	aga	cag	tac		912
Glu	Tyr	Cys	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr		
	290					295					300						
agc	cag	cct	cag	ttt	cgc	atc	aaa	gga	ggg	ctc	ttc	gcc	gac	atc	gcc		960
Ser	Gln	Pro	Gln	Phe	Arg	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala		

305	310	315	320	
tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tcg ccc				1008
Ser His Pro Trp	Gln Ala Ala Ile Phe	Ala Lys His Arg Arg	Ser Pro	
	325	330	335	
gga gag cgg ttc ctg tgc ggg ggc ata ctc atc agc tcc tgc tgg att				1056
Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile				
	340	345	350	
ctc tct gcc gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg				1104
Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu				
	355	360	365	
acg gtg atc ttg ggc aga aca tac cgg gtg gtc cct ggc gag gag gag				1152
Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu				
	370	375	380	
cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat				1200
Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp				
	385	390	400	
gac act tac gac aat gac att gcg ctg ctg cag ctg aaa tcg gat tcg				1248
Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser				
	405	410	415	
tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc				1296
Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro				
	420	425	430	
ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc				1344
Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly				
	435	440	445	
tac ggc aag cat gag gcc ttg tct cct ttc tat tcg gag cgg ctg aag				1392
Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys				
	450	455	460	
gag gct cat gtc aga ctg tac cca tcc agc cgc tgc aca tca caa cat				1440
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His				
	465	470	475	480
tta ctt aac aga aca gtc acc gac aac atg ctg tgt gct gga gac act				1488
Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr				
	485	490	495	
cgg agc ggc ggg ccc cag gca aac ttg cac gac gcc tgc cag ggc gat				1536
Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp				
	500	505	510	
tcg gga ggc ccc ctg gtg tgt ctg aac gat ggc cgc atg act ttg gtg				1584
Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val				
	515	520	525	
ggc atc atc agc tgg ggc ctg ggc tgt gga cag aag gat gtc ccg ggt				1632
Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly				
	530	535	540	

gtg tac acc aag gtt acc aac tac cta gac tgg att cgt gac aac atg 1680
Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
545 550 555 560

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<210> 12
<211> 1158
<212> DNA
<213> Artificial Sequence
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<220>
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<222> (76) ... (312)
<223> Coding sequence of the mature surfactant protein B
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<220>
<221> CDS
<222> (1141) ... (1158)
<223> Hexahistidin affinity tag
```

atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg 48
Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1 5 10 15

tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc 144
Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro
35 40 45

ctg	gtg	gcg	ggc	ggc	atc	tgc	cag	tgc	ctg	gct	gag	cgc	tac	tcc	gtc	240
Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	
65					70					75					80	

Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	
				85					90					95		
cgc	ctc	gtc	ctc	cgg	tgc	tcc	atg	aag	ccc	tcc	tct	cct	cca	gaa	gaa	336
Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	
			100					105					110			
tta	aaa	ttt	cag	tgt	ggc	caa	aag	act	ctg	agg	ccc	cgc	ttt	aag	att	384
Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	
		115					120					125				
att	ggg	gga	gaa	ttc	acc	acc	atc	gag	aac	cag	ccc	tgg	ttt	gcg	gcc	432
Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	
	130					135					140					
atc	tac	agg	agg	cac	cgg	ggg	ggc	tct	gtc	acc	tac	gtg	tgt	gga	ggc	480
Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	
145				150					155					160		
agc	ctc	atc	agc	cct	tgc	tgg	gtg	atc	agc	gcc	aca	cac	tgc	ttc	att	528
Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	
				165				170						175		
gat	tac	cca	aag	aag	gag	gac	tac	atc	gtc	tac	ctg	ggt	cgc	tca	agg	576
Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	
			180					185					190			
ctt	aac	tcc	aac	acg	caa	ggg	gag	atg	aag	ttt	gag	gtg	gaa	aac	ctc	624
Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	
		195					200					205				
atc	cta	cac	aag	gac	tac	agc	gct	gac	acg	ctt	gct	cac	cac	aac	gac	672
Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	
	210					215					220					
att	gcc	ttg	ctg	aag	atc	cgt	tcc	aag	gag	ggc	agg	tgt	gcg	cag	cca	720
Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	
225					230					235					240	
tcc	cgg	act	ata	cag	acc	atc	tgc	ctg	ccc	tgc	atg	tat	aac	gat	ccc	768
Ser	Arg	Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	
				245					250					255		
cag	ttt	ggc	aca	agc	tgt	gag	atc	act	ggc	ttt	gga	aaa	gag	aat	tct	816
Gln	Phe	Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	
			260					265					270			
acc	gac	tat	ctc	tat	ccg	gag	cag	ctg	aaa	atg	act	gtt	gtg	aag	ctg	864
Thr	Asp	Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	
			275				280					285				
att	tcc	cac	cgg	gag	tgt	cag	cag	ccc	cac	tac	tac	ggc	tct	gaa	gtc	912
Ile	Ser	His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	
	290					295					300					
acc	acc	aaa	atg	ctg	tgt	gct	gct	gac	cca	cag	tgg	aaa	aca	gat	tcc	960
Thr	Thr	Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	

305	310	315	320	
tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc				1008
Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg	325	330	335	
atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag				1056
Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys	340	345	350	
gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc				1104
Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile	355	360	365	
cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat				1152
Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His	370	375	380	
cat cat				1158
His His				
385				

<210> 13
 <211> 1149
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> sig_peptide
 <222> (1) ... (60)
 <223> Signal sequence of the urokinase plasminogen activator

 <220>
 <221> CDS
 <222> (67) ... (894)
 <223> Coding sequence of low mw two-chain urokinase-plasminogen activator

<220>
 <221> CDS
 <222> (895) ... (1131)
 <223> Coding sequence of the mature surfactant protein B

<220>
 <221> CDS
 <222> (1132) ... (1149)
 <223> Hexahistidin affinity tag

<400> 13

atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc	48
Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser	
1 5 10 15	
gac tcc aaa ggc agc aat aag ccc tcc tct cct cca gaa gaa tta aaa	96
Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys	
20 25 30	

ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att att ggg Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly 35 40 45	144
gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc atc tac Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr 50 55 60	192
agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc agc ctc Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu 65 70 75 80	240
atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att gat tac Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp Tyr 85 90 95	288
cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg ctt aac Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn 100 105 110	336
tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc atc cta Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu 115 120 125	384
cac aag gac tac agc gct gac acg ctt gct cac cac aac gac att gcc His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala 130 135 140	432
ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca tcc cgg Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg 145 150 155 160	480
act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc cag ttt Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe 165 170 175	528
ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct acc gac Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp 180 185 190	576
tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg att tcc Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser 195 200 205	624
cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc acc acc His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr 210 215 220	672
aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc tgc cag Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln 225 230 235 240	720
gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc atg act Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr 245 250 255	768

ttg act gga att gtg agc tgg	ggc cgt gga tgt gcc ctg aag gac aag	816
Leu Thr Gly Ile Val Ser Trp	Gly Arg Gly Cys Ala Leu Lys Asp Lys	
260	265 270	
cca ggc gtc tac acg aga gtc	tca cac ttc tta ccc tgg atc cgc agt	864
Pro Gly Val Tyr Thr Arg Val	Ser His Phe Leu Pro Trp Ile Arg Ser	
275	280 285	
cac acc aag gaa gag aat ggc	ctg gcc ctc ttc ccc att cct ctc ccc	912
His Thr Lys Glu Gln Asn Gly	Leu Ala Leu Phe Pro Ile Pro Leu Pro	
290	295 300	
tat tgc tgg ctc tgc agg gct	ctg atc aag cgg atc caa gcc atg att	960
Tyr Cys Trp Leu Cys Arg Ala	Leu Ile Lys Arg Ile Gln Ala Met Ile	
305	310 315 320	
ccc aag ggt gcg cta gct gtg	gca gtg gcc cag gtg tgc cgc gtg gta	1008
Pro Lys Gly Ala Leu Ala Val	Ala Val Ala Gln Val Cys Arg Val Val	
325	330 335	
cct ctg gtg gcg ggc ggc atc	tgc cag tgc ctg gct gag cgc tac tcc	1056
Pro Leu Val Ala Gly Gly Ile	Cys Gln Cys Leu Ala Glu Arg Tyr Ser	
340	345 350	
gtc atc ctg ctc gac acg ctg	ctg ggc cgc atg ctg ccc cag ctg gtc	1104
Val Ile Leu Leu Asp Thr Leu	Leu Gly Arg Met Leu Pro Gln Leu Val	
355	360 365	
tgc cgc ctc gtc ctc cgg tgc	tcc atg cat cat cat cat cat cat	1149
Cys Arg Leu Val Leu Arg Cys	Ser Met His His His His His His	
370	375 380	

<210> 14

<211> 381

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (381)

<223> Surfactant protein B precursor

<400> 14

Met Ala Glu Ser His Leu Leu	Gln Trp Leu Leu Leu Leu Pro Thr
1	5 10 15
Leu Cys Gly Pro Gly Thr Ala	Ala Trp Thr Thr Ser Ser Leu Ala Cys
20	25 30
Ala Gln Gly Pro Glu Phe Trp	Cys Gln Ser Leu Glu Gln Ala Leu Gln
35	40 45
Cys Arg Ala Leu Gly His Cys	Leu Gln Glu Val Trp Gly His Val Gly
50	55 60

Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn	65	70	75	80
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu	85	90	95	
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys	100	105	110	
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln	115	120	125	
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys	130	135	140	
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu	145	150	155	160
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu	165	170	175	
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His	180	185	190	
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys	195	200	205	
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys	210	215	220	
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu	225	230	235	240
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile	245	250	255	
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg	260	265	270	
Leu	Val	Leu	Arg	Cys	Ser	Met	Asp	Asp	Ser	Ala	Gly	Pro	Arg	Ser	Pro	275	280	285	
Thr	Gly	Glu	Trp	Leu	Pro	Arg	Asp	Ser	Glu	Cys	His	Leu	Cys	Met	Ser	290	295	300	
Val	Thr	Thr	Gln	Ala	Gly	Asn	Ser	Ser	Glu	Gln	Ala	Ile	Pro	Gln	Ala	305	310	315	320
Met	Leu	Gln	Ala	Cys	Val	Gly	Ser	Trp	Leu	Asp	Arg	Glu	Lys	Cys	Lys	325	330	335	
Gln	Phe	Val	Glu	Gln	His	Thr	Pro	Gln	Leu	Leu	Thr	Leu	Val	Pro	Arg	340	345	350	
Gly	Trp	Asp	Ala	His	Thr	Thr	Cys	Gln	Ala	Leu	Gly	Val	Cys	Gly	Thr	355	360	365	

Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu
 370 375 380

<210> 15
 <211> 279
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (279)
 <223> Surfactant protein B precursor lacking the C-terminal propeptide

<400> 15

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
 1 5 10 15
 Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
 20 25 30
 Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
 35 40 45
 Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
 50 55 60
 Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
 65 70 75 80
 Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
 85 90 95
 Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
 100 105 110
 Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
 115 120 125
 Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
 130 135 140
 Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
 145 150 155 160
 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
 165 170 175
 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
 180 185 190
 Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
 195 200 205
 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys

210	215	220
Gly Ala Leu Ala Val	Ala Val Ala Gln Val	Cys Arg Val Val Pro Leu
225	230	235 240
Val Ala Gly Gly Ile	Cys Gln Cys Leu Ala Glu Arg Tyr Ser	Val Ile
	245	250 255
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg		
	260	265 270
Leu Val Leu Arg Cys Ser Met		
	275	

<210> 16
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (79)
 <223> Mature surfactant protein B

<400> 16

Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
1 5 10 15
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
20 25 30
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
35 40 45
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
50 55 60
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
65 70 75

<210> 17
 <211> 431
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (431)
 <223> Single-chain urokinase-plasminogen activator

<400> 17

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1 5 10 15

Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
 20 25 30
 Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
 35 40 45
 His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
 50 55 60
 Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
 65 70 75 80
 Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
 85 90 95
 Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu
 100 105 110
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg
 115 120 125
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln
 130 135 140
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro
 145 150 155 160
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg
 165 170 175
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp
 180 185 190
 Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val
 195 200 205
 Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His
 210 215 220
 Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly
 225 230 235 240
 Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val
 245 250 255
 Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His
 260 265 270
 His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys
 275 280 285
 Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr
 290 295 300
 Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys
 305 310 315 320

115		120		125
Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys				
130		135		140
Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile				
145		150		155
Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln				
	165		170	175
Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln				
	180		185	190
Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala				
	195		200	205
Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro				
	210		215	220
Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser				
	225		230	235
Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg				
	245		250	255
Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn				
	260		265	270
Gly Leu Ala Leu				
	275			

<210> 19
 <211> 557
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> PEPTIDE
 <222> (1) ... (279)
 <223> Surfactant protein B precursor lacking the C-terminal propeptide

<220>
 <221> PEPTIDE
 <222> (282) ... (577)
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 19

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr				
1		5		10
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys				
	20		25	30
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln				

35					40					45					
Cys	Arg	Ala	Leu	Gly	His	Cys	Leu	Gln	Glu	Val	Trp	Gly	His	Val	Gly
50					55					60					
Ala	Asp	Asp	Leu	Cys	Gln	Glu	Cys	Glu	Asp	Ile	Val	His	Ile	Leu	Asn
65					70					75					80
Lys	Met	Ala	Lys	Glu	Ala	Ile	Phe	Gln	Asp	Thr	Met	Arg	Lys	Phe	Leu
				85					90					95	
Glu	Gln	Glu	Cys	Asn	Val	Leu	Pro	Leu	Lys	Leu	Leu	Met	Pro	Gln	Cys
			100					105					110		
Asn	Gln	Val	Leu	Asp	Asp	Tyr	Phe	Pro	Leu	Val	Ile	Asp	Tyr	Phe	Gln
		115					120					125			
Asn	Gln	Thr	Asp	Ser	Asn	Gly	Ile	Cys	Met	His	Leu	Gly	Leu	Cys	Lys
		130				135					140				
Ser	Arg	Gln	Pro	Glu	Pro	Glu	Gln	Glu	Pro	Gly	Met	Ser	Asp	Pro	Leu
145					150					155					160
Pro	Lys	Pro	Leu	Arg	Asp	Pro	Leu	Pro	Asp	Pro	Leu	Leu	Asp	Lys	Leu
				165					170					175	
Val	Leu	Pro	Val	Leu	Pro	Gly	Ala	Leu	Gln	Ala	Arg	Pro	Gly	Pro	His
			180					185					190		
Thr	Gln	Asp	Leu	Ser	Glu	Gln	Gln	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	Cys
		195					200					205			
Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	Lys
		210				215					220				
Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	Leu
225					230					235					240
Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	Ile
				245					250					255	
Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	Arg
			260					265					270		
Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Leu	Lys	Pro	Ser	Ser	Pro	Pro	Glu
			275				280					285			
Glu	Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys
				290		295					300				
Ile	Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala
305					310					315					320
Ala	Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly
				325					330					335	
Gly	Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe

340	345	350
Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser		
355	360	365
Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn		
370	375	380
Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn		
385	390	395
Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln		
405	410	415
Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp		
420	425	430
Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn		
435	440	445
Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys		
450	455	460
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu		
465	470	475
Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp		
485	490	495
Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly		
500	505	510
Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu		
515	520	525
Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp		
530	535	540
Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu		
545	550	555

<210> 20

<211> 558

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1) ... (279)

<223> Surfactant protein B precursor lacking the C-terminal propeptide

<220>

<221> PEPTIDE

<222> (283) ... (558)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 20

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1 5 10 15
Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
20 25 30
Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
35 40 45
Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
50 55 60
Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65 70 75 80
Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
85 90 95
Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
100 105 110
Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
115 120 125
Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
130 135 140
Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
145 150 155 160
Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
165 170 175
Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
180 185 190
Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
195 200 205
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
210 215 220
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
225 230 235 240
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
245 250 255
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
260 265 270
Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro
275 280 285
Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe

290	295	300
Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe 305 310 315 320		
Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys 325 330 335		
Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys 340 345 350		
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg 355 360 365		
Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu 370 375 380		
Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His 385 390 395 400		
Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala 405 410 415		
Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn 420 425 430		
Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu 435 440 445		
Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val 450 455 460		
Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser 465 470 475 480		
Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr 485 490 495		
Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln 500 505 510		
Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala 515 520 525		
Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro 530 535 540		
Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu 545 550 555		

<210> 21
 <211> 197
 <212> PRT
 <213> Homo sapiens
 <220>

<221> PEPTIDE

<222> (1) ... (197)

<223> Surfactant protein C precursor

<400> 21

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
1 5 10 15
Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
20 25 30
Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val
35 40 45
Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His
50 55 60
Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln
65 70 75 80
Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile
85 90 95
Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala
100 105 110
Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro
115 120 125
Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe
130 135 140
Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys
145 150 155 160
Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly
165 170 175
Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val
180 185 190
Pro Leu Tyr Tyr Ile
195

<210> 22

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (58)

<223> Surfactant protein C precursor lacking the C-terminal propeptide

<400> 22

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
 1 5 10 15
 Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
 20 25 30
 Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val
 35 40 45
 Val Ile Val Gly Ala Leu Leu Met Gly Leu
 50 55

<210> 23
 <211> 35
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (35)
 <223> Mature surfactant protein C

<400> 23

Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val
 1 5 10 15
 Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu
 20 25 30
 Met Gly Leu
 35

<210> 24
 <211> 562
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (562)
 <223> Tissue-plasminogen activator

<400> 24

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
 1 5 10 15
 Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
 20 25 30
 Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
 35 40 45

Ile	Tyr	Gln	Gln	His	Gln	Ser	Trp	Leu	Arg	Pro	Val	Leu	Arg	Ser	Asn	50	55	60
Arg	Val	Glu	Tyr	Cys	Trp	Cys	Asn	Ser	Gly	Arg	Ala	Gln	Cys	His	Ser	65	70	75
Val	Pro	Val	Lys	Ser	Cys	Ser	Glu	Pro	Arg	Cys	Phe	Asn	Gly	Gly	Thr	85	90	95
Cys	Gln	Gln	Ala	Leu	Tyr	Phe	Ser	Asp	Phe	Val	Cys	Gln	Cys	Pro	Glu	100	105	110
Gly	Phe	Ala	Gly	Lys	Cys	Cys	Glu	Ile	Asp	Thr	Arg	Ala	Thr	Cys	Tyr	115	120	125
Glu	Asp	Gln	Gly	Ile	Ser	Tyr	Arg	Gly	Thr	Trp	Ser	Thr	Ala	Glu	Ser	130	135	140
Gly	Ala	Glu	Cys	Thr	Asn	Trp	Asn	Ser	Ser	Ala	Leu	Ala	Gln	Lys	Pro	145	150	155
Tyr	Ser	Gly	Arg	Arg	Pro	Asp	Ala	Ile	Arg	Leu	Gly	Leu	Gly	Asn	His	165	170	175
Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Arg	Asp	Ser	Lys	Pro	Trp	Cys	Tyr	Val	180	185	190
Phe	Lys	Ala	Gly	Lys	Tyr	Ser	Ser	Glu	Phe	Cys	Ser	Thr	Pro	Ala	Cys	195	200	205
Ser	Glu	Gly	Asn	Ser	Asp	Cys	Tyr	Phe	Gly	Asn	Gly	Ser	Ala	Tyr	Arg	210	215	220
Gly	Thr	His	Ser	Leu	Thr	Glu	Ser	Gly	Ala	Ser	Cys	Leu	Pro	Trp	Asn	225	230	235
Ser	Met	Ile	Leu	Ile	Gly	Lys	Val	Tyr	Thr	Ala	Gln	Asn	Pro	Ser	Ala	245	250	255
Gln	Ala	Leu	Gly	Leu	Gly	Lys	His	Asn	Tyr	Cys	Arg	Asn	Pro	Asp	Gly	260	265	270
Asp	Ala	Lys	Pro	Trp	Cys	His	Val	Leu	Lys	Asn	Arg	Arg	Leu	Thr	Trp	275	280	285
Glu	Tyr	Cys	Asp	Val	Pro	Ser	Cys	Ser	Thr	Cys	Gly	Leu	Arg	Gln	Tyr	290	295	300
Ser	Gln	Pro	Gln	Phe	Arg	Ile	Lys	Gly	Gly	Leu	Phe	Ala	Asp	Ile	Ala	305	310	315
Ser	His	Pro	Trp	Gln	Ala	Ala	Ile	Phe	Ala	Lys	His	Arg	Arg	Ser	Pro	325	330	335
Gly	Glu	Arg	Phe	Leu	Cys	Gly	Gly	Ile	Leu	Ile	Ser	Ser	Cys	Trp	Ile	340	345	350

Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu
 355 360 365
 Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu
 370 375 380
 Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp
 385 390 395 400
 Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
 405 410 415
 Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
 420 425 430
 Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
 435 440 445
 Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
 450 455 460
 Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
 465 470 475 480
 Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
 485 490 495
 Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
 500 505 510
 Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
 515 520 525
 Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
 530 535 540
 Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
 545 550 555 560
 Arg Pro

<210> 25
 <211> 386
 <212> PRT
 <213> Artificial Sequence

 <220>
 <221> SIGNAL
 <222> (1) ... (23)
 <223> Signal sequence of the surfactant protein B

 <220>
 <221> PEPTIDE
 <222> (26) ... (104)
 <223> Mature surfactant protein B

<220>
 <221> PEPTIDE
 <222> (105) ... (380)
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> PEPTIDE
 <222> (381) ... (386)
 <223> Hexahistidin affinity tag

<400> 25

Met	Ala	Glu	Ser	His	Leu	Leu	Gln	Trp	Leu	Leu	Leu	Leu	Leu	Pro	Thr	1	5	10	15
Leu	Cys	Gly	Pro	Gly	Thr	Ala	Ala	Trp	Phe	Pro	Ile	Pro	Leu	Pro	Tyr	20	25	30	
Cys	Trp	Leu	Cys	Arg	Ala	Leu	Ile	Lys	Arg	Ile	Gln	Ala	Met	Ile	Pro	35	40	45	
Lys	Gly	Ala	Leu	Ala	Val	Ala	Val	Ala	Gln	Val	Cys	Arg	Val	Val	Pro	50	55	60	
Leu	Val	Ala	Gly	Gly	Ile	Cys	Gln	Cys	Leu	Ala	Glu	Arg	Tyr	Ser	Val	65	70	75	80
Ile	Leu	Leu	Asp	Thr	Leu	Leu	Gly	Arg	Met	Leu	Pro	Gln	Leu	Val	Cys	85	90	95	
Arg	Leu	Val	Leu	Arg	Cys	Ser	Met	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	100	105	110	
Leu	Lys	Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	115	120	125	
Ile	Gly	Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	130	135	140	
Ile	Tyr	Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	145	150	155	160
Ser	Leu	Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	165	170	175	
Asp	Tyr	Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	180	185	190	
Leu	Asn	Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	195	200	205	
Ile	Leu	His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	210	215	220	
Ile	Ala	Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	225	230	235	240

Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro
 245 250 255
 Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser
 260 265 270
 Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu
 275 280 285
 Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val
 290 295 300
 Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser
 305 310 315 320
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg
 325 330 335
 Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys
 340 345 350
 Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile
 355 360 365
 Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His
 370 375 380
 His His
 385

<210> 26
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1) ... (20)
 <223> Signal sequence of the urokinase plasminogen activator

<220>
 <221> PEPTIDE
 <222> (23) ... (298)
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> PEPTIDE
 <222> (299) ... (377)
 <223> Coding sequence of the mature surfactant protein B

<220>
 <221> PEPTIDE
 <222> (378) ... (383)
 <223> Hexahistidin affinity tag

<400> 26

Met	Arg	Ala	Leu	Leu	Ala	Arg	Leu	Leu	Leu	Cys	Val	Leu	Val	Val	Ser	1	5	10	15
Asp	Ser	Lys	Gly	Ser	Asn	Lys	Pro	Ser	Ser	Pro	Pro	Glu	Glu	Leu	Lys	20	25	30	
Phe	Gln	Cys	Gly	Gln	Lys	Thr	Leu	Arg	Pro	Arg	Phe	Lys	Ile	Ile	Gly	35	40	45	
Gly	Glu	Phe	Thr	Thr	Ile	Glu	Asn	Gln	Pro	Trp	Phe	Ala	Ala	Ile	Tyr	50	55	60	
Arg	Arg	His	Arg	Gly	Gly	Ser	Val	Thr	Tyr	Val	Cys	Gly	Gly	Ser	Leu	65	70	75	80
Ile	Ser	Pro	Cys	Trp	Val	Ile	Ser	Ala	Thr	His	Cys	Phe	Ile	Asp	Tyr	85	90	95	
Pro	Lys	Lys	Glu	Asp	Tyr	Ile	Val	Tyr	Leu	Gly	Arg	Ser	Arg	Leu	Asn	100	105	110	
Ser	Asn	Thr	Gln	Gly	Glu	Met	Lys	Phe	Glu	Val	Glu	Asn	Leu	Ile	Leu	115	120	125	
His	Lys	Asp	Tyr	Ser	Ala	Asp	Thr	Leu	Ala	His	His	Asn	Asp	Ile	Ala	130	135	140	
Leu	Leu	Lys	Ile	Arg	Ser	Lys	Glu	Gly	Arg	Cys	Ala	Gln	Pro	Ser	Arg	145	150	155	160
Thr	Ile	Gln	Thr	Ile	Cys	Leu	Pro	Ser	Met	Tyr	Asn	Asp	Pro	Gln	Phe	165	170	175	
Gly	Thr	Ser	Cys	Glu	Ile	Thr	Gly	Phe	Gly	Lys	Glu	Asn	Ser	Thr	Asp	180	185	190	
Tyr	Leu	Tyr	Pro	Glu	Gln	Leu	Lys	Met	Thr	Val	Val	Lys	Leu	Ile	Ser	195	200	205	
His	Arg	Glu	Cys	Gln	Gln	Pro	His	Tyr	Tyr	Gly	Ser	Glu	Val	Thr	Thr	210	215	220	
Lys	Met	Leu	Cys	Ala	Ala	Asp	Pro	Gln	Trp	Lys	Thr	Asp	Ser	Cys	Gln	225	230	235	240
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Ser	Leu	Gln	Gly	Arg	Met	Thr	245	250	255	
Leu	Thr	Gly	Ile	Val	Ser	Trp	Gly	Arg	Gly	Cys	Ala	Leu	Lys	Asp	Lys	260	265	270	
Pro	Gly	Val	Tyr	Thr	Arg	Val	Ser	His	Phe	Leu	Pro	Trp	Ile	Arg	Ser	275	280	285	
His	Thr	Lys	Glu	Gln	Asn	Gly	Leu	Ala	Leu	Phe	Pro	Ile	Pro	Leu	Pro	290	295	300	

Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile
305 310 315 320

Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val
325 330 335

Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser
340 345 350

Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val
355 360 365

Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His
370 375 380